REMARKS

Prior to this amendment claims 1-26 were pending. Claims 1-26 are canceled. Claims 27-39 are new. Support for new claims 27 and 32 is found at p. 7, lines 20-25, and p. 29, line 35-p. 30, line 27. Support for the remaining new claims is found throughout the specification and in the claims as filed. Applicants submit that no new matter is introduced by way of this amendment. For the Examiner's convenience, a copy of the currently pending claims is attached hereto as Appendix A. A copy of the "Version to Show Changes Made" is also attached as Appendix B.

Priority

Applicants see that the Examiner asserts that the applications upon which priority is claimed fail to provide adequate support for claims 2, 6, 13, 15, 16-18 and 25. In reply, Applicants note that these claims are canceled herein. With respect to the new claims, Applicants draw the Examiner's attention to p. 31 of U.S.S.N. 60/090,473, which provides support for the claims submitted herein. As such, Applicants submit that the instant claims find support in U.S.S.N. 60/090,473 and should be given the benefit of the June 24, 1998 filing date as claimed.

Information Disclosure Statement

Applicants appreciate the Examiner's attention to the information disclosure statements and Statement of Relatedness. Applicants would like to clarify an inconsistency between remarks in the Statement of Relatedness and the claim of priority of the present application. As shown on the application transmittal and in the specification of the present application, the present application is a continuing application of 09/344,526 and 09/189,543. Applicants submit that the claims as submitted herein find support in these parent applications and that the statement that it was not believed that the invention was not disclosed in the statement of relatedness was mistaken.

Specification

The Examiner indicates that the specification contains nucleic acid sequences that do not have SEQ ID NOs. In response, Applicants have amended the specification to include a Sequence Listing and proper references to the listed sequences. Changes made to the specification in relation to the Sequence Listing are reflected in Appendix B, "Version to Show Changes Made."

Response to Rejections

35 U.S.C. § 112, second paragraph

Claims 9, 16, 23, 24 and 26 are rejected under 35 U.S.C. § 112, second paragraph. Applicants submit that in light of the amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

35 U.S.C. § 102

Claims 1, 3-5, 7-12 and 14-25 are rejected under 35 U.S.C. § 102 (b) as being anticipated by Walt et al. (U.S. Patent No. 6,023,540).

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

Claims 19-21 and 23-26 are rejected under 35 U.S.C. § 102 (e) as being anticipated by Kamb et al. (U.S. Patent No. 6,060,240).

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

35 U.S.C. § 103

Claims 2-6 and 13 are rejected under 35 U.S.C. § 103 as being unpatentable over Walt et al (6,023,540) in view of Brenner et al (U.S. Patent No. 5,863,722)

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

Claim 26 is rejected under 35 U.S.C. § 103 as being unpatentable over Walt et al (6,023,540) in view of Kamb (6,060,240).

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

Double Patenting

Claims 1, 3-5 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1, 5, 6, 12 and 13 of U.S. Patent No. 6,429,027.

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

Claims 1-7, 15-22 and 24 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-7 and 15-36 of copending Application No. 09/189,543.

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

Claims 8-14 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting a being unpatentable over claims 8-14, 16-28 and 30-35 of copending Application No. 09/344,526.

In response Applicants submit that in light of the claim amendments submitted herein the rejection is moot. Applicants respectfully request the Examiner to withdraw the rejection.

CONCLUSION

Applicants submit that the claims are in condition for allowance, and early notification to this effect is solicited. Applicants submit that the amended specification, the accompanying paper copy of the Sequence Listing and letter requesting use of a previously filed computer readable form of the Sequence Listing serve to place this application in a condition of compliance with the rules 37 C.F.R. §§ 1.821-1.825. The Examiner is invited to contact the undersigned at (415) 781-1989 if any issues remain.

Respectfully submitted,

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Appendix A

Pending Claims

27. (New) A method of decoding an array composition comprising:

a) providing an array comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least first and second subpopulations, wherein each subpopulation comprises a distinct capture probe, randomly distributed on said sites;

b) providing a population of decoding probes wherein each of said decoding probes is complementary to one of said capture probes;

c) dividing said population into a plurality of first sets wherein each of said first sets is labeled with a different label;

d) obtaining a first image by:

i) hybridizing said first sets to said capture probes; and

ii) detecting the signal at each location in the array;

e) dividing said population into a plurality of second sets, wherein said first and second sets are different, and each of said second sets is labeled with a different label;

f) obtaining a second image by:

i) hybridizing said second sets to said capture probes; and

ii) detecting the signal at each location in the array; and

g) analyzing said first image and said second image to decode said array.

28. (New) The method according to claim 27, further comprising:

g) optionally repeating steps e), f) and g) to decode said array.

29. (New) The method according to claim 27 or 28, wherein said microspheres comprise bioactive agent.

30. (New) The method according to claim 29, wherein at least one of said bioactive agents is a nucleic acid.

31. (New) The method according to claim 29, wherein at least one of said bioactive agents is a protein.

32. (New) A method of decoding an array comprising:

a) contacting an array comprising a population of microspheres comprising a plurality of subpopulations, wherein each subpopulation comprises a distinct bioactive agent, with a first plurality of labeled decoding binding ligands,

b) obtaining a first image of the location of each of said first population of labeled decoding binding ligands;

c) removing said first population of labeled decoding binding ligands;

d) contacting said array with a second plurality of labeled decoding binding ligands;

e) obtaining a second image of the location of each of said second population of labeled decoding binding ligands;

f) analyzing said first and second image to decode said array.

33. (New) The method according to claim 32, whereby the number of labels in said first or second plurality of labeled decoding binding ligands is less than the number of subpopulations of microspheres.

34. (New) The method according to claim 32, whereby said first and second plurality of labeled decoding binding ligands comprise the same population of decoding binding ligands, but are labeled differently.

35. (New) The method according to claim 32, wherein at least one of said bioactive agents is a nucleic acid.

36. (New) The method according to claim 32, wherein at least one of said bioactive agents is a protein.

37. (New) The method according to claim 32, wherein said microspheres are distributed in a substrate comprising a surface with discrete sites.

38. (New) The method according to claim 27 or 37, wherein said substrate is selected from the group consisting of glass, plastic and fiber optic bundle.

39. (New) The method according to claim 27 or 32, wherein said labels are fluorescent labels.

Appendix B -- Version To Show Changes Made

In the Claims:

Cancel claims 1-26.

The following claims are new:

27. (New) A method of decoding an array composition comprising:

a) providing an array comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least first and second subpopulations, wherein each subpopulation comprises a distinct capture probe, randomly distributed on said sites;

b) providing a population of decoding probes wherein each of said decoding probes is complementary to one of said capture probes;

c) dividing said population into a plurality of first sets wherein each of said first sets is labeled with a different label;

d) obtaining a first image by:

i) hybridizing said first sets to said capture probes; and

ii) detecting the signal at each location in the array;

e) dividing said population into a plurality of second sets, wherein said first and second sets are different, and each of said second sets is labeled with a different label;

f) obtaining a second image by:

i) hybridizing said second sets to said capture probes; and

ii) detecting the signal at each location in the array; and

g) analyzing said first image and said second image to decode said array.

28. (New) The method according to claim 27, further comprising:

g) optionally repeating steps e), f) and g) to decode said array.

29. (New) The method according to claim 27 or 28, wherein said microspheres comprise bioactive agent.

30. (New) The method according to claim 29, wherein at least one of said bioactive agents is a nucleic acid.

31. (New) The method according to claim 29, wherein at least one of said bioactive agents is a protein.

32. (New) A method of decoding an array comprising:

a) contacting an array comprising a population of microspheres comprising a plurality of subpopulations, wherein each subpopulation comprises a distinct bioactive agent, with a first plurality of labeled decoding binding ligands,

b) obtaining a first image of the location of each of said first population of labeled decoding binding ligands;

c) removing said first population of labeled decoding binding ligands;

d) contacting said array with a second plurality of labeled decoding binding ligands;

e) obtaining a second image of the location of each of said second population of labeled decoding binding ligands;

f) analyzing said first and second image to decode said array.

33. (New) The method according to claim 32, whereby the number of labels in said first or second plurality of labeled decoding binding ligands is less than the number of subpopulations of microspheres.

34. (New) The method according to claim 32, whereby said first and second plurality of labeled decoding binding ligands comprise the same population of decoding binding ligands, but are labeled differently.

35. (New) The method according to claim 32, wherein at least one of said bioactive agents is a nucleic acid.

36. (New) The method according to claim 32, wherein at least one of said bioactive agents is a protein.

37. (New) The method according to claim 32, wherein said microspheres are distributed in a substrate comprising a surface with discrete sites.

38. (New) The method according to claim 27 or 37, wherein said substrate is selected from the group consisting of glass, plastic and fiber optic bundle.

39. (New) The method according to claim 27 or 32, wherein said labels are fluorescent labels.

In the Specification:

The paragraph beginning at page 6, line 1, was amended to read as follows:

Figure 5 Use of fluorescence resonance energy transfer to discriminate between linkers of varying length (SEQ ID NOS:1-6).

The paragraph beginning at page 64, line 27, was amended to read as follows:

Example 5

The following FRET oligonucleotides (probes ET1, ET2, ET5 and ET7) were synthesized as is known in the art and labeled with Cy3 and fluorscein separated by linkers of varying length:

ET1 T**G*CACGAGAATGGAGGTATCT (SEQ ID NO:1)

ET2 C**TGTCGC*ACGAGAATGGAGGTATCT (SEQ ID NO:2)

ET5 C**TGTCGGGGCACTCATTTGTGC*ACGAGAATGGAGGTATCT (SEQ ID NO:5)

ET7 C**TGTCGGGGCACTCATTTGTCTGTCGGGGCGC*ACGAGAATGGAGGTATCT. (SEQ ID NO:6)

**is Cy3 * is fluorescein

The enclosed 2-page text entitled "Sequence Listing" was inserted into the specification preceding the section entitled "Claims."